

1/3) 0420



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RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/09/896,856

TIME: 19:05:04

Input Set : N:\Crf3\RULE60\09896856.txt

Output Set: N:\CRF3\02142002\I896856.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Baker, Joffre

6 Chien, Kenneth

7 King, Kathleen

8 Pennica, Diane

9 Wood, William

11 (ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

13 (iii) NUMBER OF SEQUENCES: 8

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Genentech, Inc.

17 (B) STREET: 460 Point San Bruno Blvd

18 (C) CITY: South San Francisco

19 (D) STATE: California

20 (E) COUNTRY: USA

21 (F) ZIP: 94080

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: WinPatin (Genentech)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/896,856

C--> 31 (B) FILING DATE: 29-Jun-2001

42 (C) CLASSIFICATION:

53 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 08/733,850

36 (B) FILING DATE: 18-OCT-1996

40 (A) APPLICATION NUMBER: US 08/471,112

41 (B) FILING DATE: 06-JUN-1995

46 (A) APPLICATION NUMBER: 08/233,609

47 (B) FILING DATE: 25-APR-1994

50 (A) APPLICATION NUMBER: 08/286304

51 (B) FILING DATE: 05-AUG-1994

54 (A) APPLICATION NUMBER: 08/443129

55 (B) FILING DATE: 17-MAY-1995

57 (viii) ATTORNEY/AGENT INFORMATION:

58 (A) NAME: Conley, Deirdre L.

59 (B) REGISTRATION NUMBER: 36,487

60 (C) REFERENCE/DOCKET NUMBER: P0894P1D2C1

62 (ix) TELECOMMUNICATION INFORMATION:

63 (A) TELEPHONE: 415/225-2066

64 (B) TELEFAX: 415/952-9881

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65         (C) TELEX: 910/371-7168
67 (2) INFORMATION FOR SEQ ID NO: 1:
69     (i) SEQUENCE CHARACTERISTICS:
70         (A) LENGTH: 1352 base pairs
71         (B) TYPE: Nucleic Acid
72         (C) STRANDEDNESS: Single
73         (D) TOPOLOGY: Linear
75     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC 50
80 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100
82 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAAC 150
84 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT 200
86 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250
88 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300
90 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC 350
92 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400
94 CAGGTTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450
96 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT 500
98 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550
100 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600
102 GGGCCAGCTG GTGCCAGGGG GCGTCGCCCTG AGAGTGAATA CTTTTCTCTG 650
104 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT 700
106 CTGTGTCTCT TGTTCTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG 750
108 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800
110 TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC 850
112 TCTTTTGTGT TCCTTGCTCT TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900
114 GCTTGCTTGT TGTGAGACA GGTCTCACC ATATAGCTCT GGATGGCCTG 950
116 GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000
118 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050
120 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100
122 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA 1150
124 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCCTTGTA GGCAAAATCCC 1200
126 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA 1250
128 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300
130 AATTTTGTGA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350
132 AA 1352
134 (2) INFORMATION FOR SEQ ID NO: 2:
136     (i) SEQUENCE CHARACTERISTICS:
137         (A) LENGTH: 1352 base pairs
138         (B) TYPE: Nucleic Acid
139         (C) STRANDEDNESS: Single
140         (D) TOPOLOGY: Linear
142     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
145 CCTATTCGGA CCCCGTCTG ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50
147 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100
149 GCGGTCTGTG TGTGGAACG GCGGAGGAC TGGTTTATAC GTCTTGTTGA 150
151 AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200
153 AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250
155 GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA 300

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157 CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG 350
159 ACTTGGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400
161 GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGC GCGACCC 450
163 GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CCGTGGGAGA 500
165 AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550
167 GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA 600
169 CCCGGTTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC 650
171 ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700
173 GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC 750
175 AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800
177 AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG 850
179 AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA 900
181 CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950
183 CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC 1000
185 GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA 1050
187 CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA 1100
189 AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150
191 TCCGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200
193 AGGGGGAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250
195 CTCTCTTCC GTCTTTTGT AGAAATTTCT CAAATAAAC TCTTATTTAA 1300
197 TTAATAACAT TTATTTTACA AATTGTTATT TTGATTGAA AATACTTTTT 1350
199 TT 1352

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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210 Met Ser Gln Arg Glu Gly Ser Leu Glu Asp His Gln Thr Asp Ser
211 1 5 10 15
213 Ser Ile Ser Phe Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr
214 20 25 30
216 His Asn Leu Ala Arg Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu
217 35 40 45
219 Glu Glu Tyr Val Gln Gln Gln Gly Glu Pro Phe Gly Leu Pro Gly
220 50 55 60
222 Phe Ser Pro Pro Arg Leu Pro Leu Ala Gly Leu Ser Gly Pro Ala
223 65 70 75
225 Pro Ser His Ala Gly Leu Pro Val Ser Glu Arg Leu Arg Gln Asp
226 80 85 90
228 Ala Ala Ala Leu Ser Val Leu Pro Ala Leu Leu Asp Ala Val Arg
229 95 100 105
231 Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg
232 110 115 120
234 Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala
235 125 130 135
237 Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Arg Gly Pro
238 140 145 150
240 Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser

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241		155		160		165
243	Thr Ala Gly Ile Phe Ser Ala Lys Val	Leu Gly Phe His Val Cys				
244		170		175		180
246	Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly					
247		185		190		195
249	Gln Leu Val Pro Gly Gly Val Ala					
250		200		203		

252 (2) INFORMATION FOR SEQ ID NO: 4:

254 (i) SEQUENCE CHARACTERISTICS:

255 (A) LENGTH: 200 amino acids

256 (B) TYPE: Amino Acid

257 (D) TOPOLOGY: Linear

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

261	Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp
262	1 5 10 15
264	Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp
265	20 25 30
267	Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn
268	35 40 45
270	Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser
271	50 55 60
273	Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu
274	65 70 75
276	Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu
277	80 85 90
279	Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe
280	95 100 105
282	His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala
283	110 115 120
285	Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro
286	125 130 135
288	Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
289	140 145 150
291	Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
292	155 160 165
294	Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
295	170 175 180
297	Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
298	185 190 195
300	Asn Asn Lys Lys Met
301	200

303 (2) INFORMATION FOR SEQ ID NO: 5:

305 (i) SEQUENCE CHARACTERISTICS:

306 (A) LENGTH: 50 base pairs

307 (B) TYPE: Nucleic Acid

308 (C) STRANDEDNESS: Single

309 (D) TOPOLOGY: Linear

311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

314 GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50

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Input Set : N:\Crif3\RULE60\09896856.txt

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316 (2) INFORMATION FOR SEQ ID NO: 6:

318 (i) SEQUENCE CHARACTERISTICS:

319 (A) LENGTH: 1018 base pairs

320 (B) TYPE: Nucleic Acid

321 (C) STRANDEDNESS: Single

322 (D) TOPOLOGY: Linear

324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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327 GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50
329 AGTCTGGAAG ACCCCAGAGC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100
331 GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150
333 ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200
335 GGGGTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250
337 CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300
339 ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350
341 CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCCTGA 400
343 GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCCTGC 450
345 TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCGCCCGGCC 500
347 GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550
349 GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCAGAG 600
351 GCGACCTGGG CCAGGTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC 650
353 AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700
355 GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750
357 ATTGCCTCGG CCTTCTTTGC TTTTGTGGG GGAGAGGGGA GGGGACGGGC 800
359 AGGGTCTCTG TCGCCCAGGC TGGGGTGAGC TGGCGCGATC CCAGCACTGC 850
361 AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900
363 AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA 950
365 TTTTGTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAAC 1000
367 CCGGGGCTCA AGCGATCC 1018

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369 (2) INFORMATION FOR SEQ ID NO: 7:

371 (i) SEQUENCE CHARACTERISTICS:

372 (A) LENGTH: 1018 base pairs

373 (B) TYPE: Nucleic Acid

374 (C) STRANDEDNESS: Single

375 (D) TOPOLOGY: Linear

377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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380 CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50
382 TCAGACCTTC TGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100
384 CCTCCGTTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150
386 TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200
388 CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250
390 GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300
392 TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350
394 GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400
396 CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450
398 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500
400 CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCACGA 550
402 CCCCAGGGCG CAAACGCGCG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600
404 CGCTGGACCC GGTGCGACGAC GGGCCCCCGA GCCGACTCG CGGCGCCCCG 650
406 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700

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VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]